

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101591,870A
Source: JFWO
Date Processed by STIC: 4/2/07

ENTERED



IFWO

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/591,870A

DATE: 04/02/2007
 TIME: 13:21:29

Input Set : A:\PTO.KD.txt
 Output Set: N:\CRF4\04022007\J591870A.raw

4 <110> APPLICANT: Lanahan, Mike
 6 <120> TITLE OF INVENTION: Self-processing Plants and Plant Parts
 8 <130> FILE REFERENCE: 109846.317
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,870A
 C--> 10 <141> CURRENT FILING DATE: 2006-09-07
 10 <150> PRIOR APPLICATION NUMBER: PCT/US04/07182
 11 <151> PRIOR FILING DATE: 2004-03-15
 13 <160> NUMBER OF SEQ ID NOS: 112
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 436
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: synthetic
 25 <400> SEQUENCE: 1
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 27 1 5 10 15
 28 Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
 29 20 25 30
 30 Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
 31 35 40 45
 32 Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
 33 50 55 60
 34 Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
 35 65 70 75 80
 36 Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
 37 85 90 95
 38 Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
 39 100 105 110
 40 Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
 41 115 120 125
 42 Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
 43 130 135 140
 44 Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
 45 145 150 155 160
 46 Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
 47 165 170 175
 48 Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
 49 180 185 190
 50 Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
 51 195 200 205
 52 Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr

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53 210 215 220
 54 Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
 55 225 230 235 240
 56 Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
 57 245 250 255
 58 Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
 59 260 265 270
 60 Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
 61 275 280 285
 62 His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
 63 290 295 300
 64 Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
 65 305 310 315 320
 66 Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
 67 325 330 335
 68 Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
 69 340 345 350
 70 Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
 71 355 360 365
 72 Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
 73 370 375 380
 74 Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
 75 385 390 395 400
 76 Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
 77 405 410 415
 78 Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
 79 420 425 430
 80 Cys Gly Val Gly
 81 435
 84 <210> SEQ ID NO: 2
 85 <211> LENGTH: 1308
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Artificial Sequence
 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: synthetic
 92 <400> SEQUENCE: 2
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 94 gtcccgagcg gaggcatctg gtggacacc atccgcccaga agatccccga gtggtacgac 120
 95 gccggcatct cgcgcatctg gataccgcca gcttccaagg gcatgtccgg gggctactcg 180
 96 atgggctacg acccgtaga ctacttcgac ctcggcgagt actaccagaa gggcacggtg 240
 97 gagacgcgct tcgggtccaa gcaggagctc atcaacatga tcaacacggc gcacgcctac 300
 98 ggcataagg tcatcgccga catcgatc aaccacaggg cggcgccga cctggagtgg 360
 99 aaccggctcg tcggcgacta cacctggacg gacttctcca aggtcgccctc cggcaagtac 420
 100 accggccaact acctcgactt ccacccaaac gagctgcacg cgggcgactc cggcacgttc 480
 101 ggcggctacc cggacatctg ccacgacaag tcctgggacc agtactggct ctgggcctcg 540
 102 caggagtcct acgcggccta cctgcgtcc atcggcatcg acgcgtggcg cttcgactac 600
 103 gtcaagggtc acggggcctg ggtggtcaag gactggctca actggtgccc cggctggcg 660
 104 gtggcgagt actgggacac caacgtcgac gcgctgctca actgggccta ctcctccggc 720
 105 gccaagggtgt tcgacttccc cctgtactac aagatggacg cggccttcga caacaagaac 780

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106 atcccggcgc tcgtcgaggc cctgaagaac ggccgcacgg tggctcccg cgaccggc 840
 107 aaggccgtga ctttcgtcgc caaccacgac acggacatca tctggAACaa gtacccggc 900
 108 tacgccttca tcctcaccta cgagggccag cccacgatct tctaccgcgta ctacgaggag 960
 109 tggctgaaca aggacaagct caagaacctg atctggattc acgacaacct cgcggccgc 1020
 110 tccactagta tcgtgtacta cgactccgac gagatgatct tcgtccgcaa cggctacggc 1080
 111 tccaagcccg gcctgatcac gtacatcaac ctggctcct ccaagggtgg cggctgggtg 1140
 112 tacgtcccga agttcgccgg cgcgtgcata cacgagtaca cccgcaacct cggcggctgg 1200
 113 gtggacaagt acgtgtactc ctccggctgg gtctacctgg aggcccgcc ctacgacccc 1260
 114 gccaacggcc agtacggcta ctccgtgtgg tcctactgcg gcgtcggc 1308
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 117 <211> LENGTH: 800
 118 <212> TYPE: PRT
 119 <213> ORGANISM: Artificial Sequence
 121 <220> FEATURE:
 122 <223> OTHER INFORMATION: synthetic
 124 <400> SEQUENCE: 3
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 127 Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met Asp Leu Thr
 128 20 25 30
 129 Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala Lys Asp Val
 130 35 40 45
 131 Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala Glu Val Trp
 132 50 55 60
 133 Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro Asp Thr Ser
 134 65 70 75 80
 135 Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val Ile Glu Ala
 136 85 90 95
 137 Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu Phe Lys Val
 138 100 105 110
 139 Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu Lys Ala Asp
 140 115 120 125
 141 Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val Leu Ser Glu
 142 130 135 140
 143 Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu Ile Ile Glu
 144 145 150 155 160
 145 Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu Asp Asp Tyr
 146 165 170 175
 147 Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu Lys Thr Ile
 148 180 185 190
 149 Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val Leu Leu Phe
 150 195 200 205
 151 Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn Met Glu Tyr
 152 210 215 220
 153 Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp Leu Asp Gly
 154 225 230 235 240
 155 Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile Arg Thr Thr
 156 245 250 255
 157 Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln Glu Ser Ala

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158	260	265	270
159	Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu Asn Asp Arg		
160	275	280	285
161	Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr Glu Ile His		
162	290	295	300
163	Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys Asn Lys Gly		
164	305	310	315
165	Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Gly Pro Gly Gly Val		
166	325	330	335
167	Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr His Val His		
168	340	345	350
169	Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu Asp Lys Asp		
170	355	360	365
171	Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu Phe Met Val		
172	370	375	380
173	Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His Thr Arg Ile		
174	385	390	395
175	Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His Gly Ile Gly		
176	405	410	415
177	Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile Gly Glu Leu		
178	420	425	430
179	Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg Ile Asp Lys		
180	435	440	445
181	Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val Ile Ala Ser		
182	450	455	460
183	Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val Thr Tyr Trp		
184	465	470	475
185	480	485	490
186	495	500	505
187	510	515	520
188	525	530	535
189	540	545	550
190	555	560	565
191	570	575	580
192	585	590	595
193	605	610	615
194	620	625	630
195	635	640	645
196	650	655	660

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207 Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asn Ser Tyr Asn
 208 660 665 670
 209 Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys Leu Gln Phe
 210 675 680 685
 211 Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu Arg Lys Glu
 212 690 695 700
 213 His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys Lys His Leu
 214 705 710 715 720
 215 Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met Leu Lys Asp
 216 725 730 735
 217 His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile Tyr Asn Gly
 218 740 745 750
 219 Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys Trp Asn Val
 220 755 760 765
 221 Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu Thr Val Glu
 222 770 775 780
 223 Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu Tyr Arg Glu
 224 785 790 795 800
 227 <210> SEQ ID NO: 4
 228 <211> LENGTH: 2400
 229 <212> TYPE: DNA
 230 <213> ORGANISM: Artificial Sequence
 232 <220> FEATURE:
 233 <223> OTHER INFORMATION: synthetic
 235 <400> SEQUENCE: 4
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 237 aagggtggccg tggtaagct cccgatggac ctcaccaagg tggcatcat cgtgcgcctc 120
 238 aacgagtggc aggcaagga cgtggccaag gaccgcttca tcgagatcaa ggacggcaag 180
 239 gccgaggtgt ggatactcca gggcgtggag gagatcttct acgagaagcc ggacacctcc 240
 240 cccgcgcatct tcttcgccc ggcggctcc aacaaggta tcgaggcctt cctcaccaac 300
 241 cccgtggaca ccaagaagaa ggagctgttc aaggtgaccg tcgacggcaa ggagatcccg 360
 242 gtgtcccgcg tggagaaggc cgaccgcacc gacatcgacg tgaccaacta cgtgcgcato 420
 243 gtgctctccg agtccctcaa ggaggaggac ctccgcaagg acgtggagct gatcatcgag 480
 244 ggctacaagc cggccgcgt gatcatgatg gagatctcg acgactacta ctacgacggc 540
 245 gagctggggg cgggttactc cccggagaag accatcttcc gcgtgtggc cccgggtgtcc 600
 246 aagtgggtga aggtgttctt cttcaagaac ggcgaggaca cccggcgta ccaggtggtg 660
 247 aacatggagt acaagggcaa cggcgtgtgg gagggcgtgg tggaggcgaa cctcgacggc 720
 248 gtgttctacc tctaccagct ggagaactac ggcaagatcc gcaccacgt ggacccgtac 780
 249 tccaaaggccg tgcacgccaa caaccaggag tctgcagtgg tgaacctcgc cccgcaccaac 840
 250 cccggagggt gggagaacga cccgcggcccg aagatcgagg gctacgagga cccatcatc 900
 251 tacgagatcc acatcgccga catcaccggc ctggagaact cccggcgtgaa gaacaagggc 960
 252 ctctacctcg gcctcaccga ggagaacacc aaggccccgg gcggcgtgac caccggcctc 1020
 253 tcccacctcg tggagctggg cgtgaccacatcc tcccgttctt cgacttctac 1080
 254 accggcgcacg agctggacaa ggacttcgag aagtactaca actggggcta cgacccgtac 1140
 255 ctcttcatgg tgccggaggg cccgtactcc accgaccgcga agaaccgcga caccgcatt 1200
 256 cccgaggtgtga aggagatggt gaaggccctc cacaaggcacc gcacccgtac gatcatggac 1260
 257 atgggtttcc cgcacaccta cggcatggc gagctgtccg cttcgacca gaccgtgccc 1320
 258 tactacttct accgcatcga caagaccggc gcctaccta acgagtccgg ctgcggcaac 1380
 259 gtgatcgccct ccgagcgccc gatgatgcgc aagttcatcg tggacaccgt gacctactgg 1440

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3247 M:283 W: Missing Blank Line separator, <220> field identifier